

Attorney Docket No.: 47635-0002-00-US
Application No. 10/791,791
Office Action Dated: June 13, 2008
Amendment Dated: December 11, 2008

EXHIBIT 1

Table 1 (continued)

SEQ NO	SEQ NO (DNA)	Initial (nt)	Terminal (nt)	ORF (bp)	4th Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
1743	5243	1667550	1669401	1452	gsp.W27812	Brevibacterium flavum	98.8	100.0	484	glucose-6-phosphate dehydrogenase
1744	5244	1669419	1670375	957	plr.A70917	Mycobacterium tuberculosis H37Rv Rv1448c opa	40.6	71.7	318	oxopropylate protein (glucose 6-phosphate dehydrogenase assembly protein)
1745	5245	1670395	1671099	705	sp.SOL3_YEAST	Saccharomyces cerevisiae S288C YHR163W sal3	26.7	58.1	258	6-phosphogluconolactonase
1746	5246	1671677	1671273	405	sp.SA0X_BACSN	Bacillus sp. NS-129	35.2	57.8	128	sarcosine oxidase
1747	5247	1671723	1673123	1401	gp.AF126281.1	Rhodococcus erythropolis	24.6	46.5	500	transposase (IS1676)
1748	5248	1674105	1673266	840	gp.CGL00732_5	Corynebacterium glutamicum ATCC 13052 saxA	100.0	100.0	205	sarcosine oxidase
1749	5249	1677211	1677384	174						
1750	5250	1678755	1676070	687						
1751	5251	1679148	1680128	581						
1752	5252	1681108	1680332	777	sp.TPIS_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 tpa	99.2	99.6	259	triase-phosphate isomerase
1753	5253	1681263	1681670	408	SP.YCQ3_YEAST	Saccharomyces cerevisiae YCR013c	37.0	51.0	128	probable membrane protein
1754	5254	1682404	1681190	1215	sp.PGK_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 pgk	98.0	98.5	405	phosphoglycerate kinase
1755	5255	1683625	1682624	1002	sp.G3P_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 gap	99.1	99.7	333	glyceraldehyde-3-phosphate dehydrogenase
1756	5256	1685097	1684117	981	plr.D70903	Mycobacterium tuberculosis H37Rv Rv1423	63.9	87.4	324	hypothetical protein
1757	5257	1686132	1685110	1023	sp.YR40_MYCTU	Mycobacterium tuberculosis H37Rv Rv1422	56.3	82.5	309	hypothetical protein
1758	5258	1687078	1686152	927	sp.YR39_MYCTU	Mycobacterium tuberculosis H37Rv Rv1421	52.0	76.2	281	hypothetical protein
1759	5259	1689190	1687103	2088	sp.UVRP_PSEFL	Synechocystis sp. PCC6803	34.4	61.5	701	exonuclease ABC subunit C

Table 1 (continued)

SEQ NO. [DNA]	SEQ NO. (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	MATCH length (aa)	Function
3198	6698	310734	3102768	1035	gp-SC6G4_33	Streptomyces coelicolor A3(2) SC6G4_33	31.6	57.1	380	transcriptional regulator
3199	6699	310763	3101744	120						
3200	6700	3102630	3102079	552						
3201	6701	3102894	3103763	870						
3202	6702	3103926	3104252	327	pir-B26872	Streptomyces lavendulae ORF372	43.9	81.3	107	hypothetical protein
3203	6703	3104406	3105719	1314	sp-AMVH_YEAST	Saccharomyces cerevisiae S288C YI019C sta1	28.7	55.3	432	glucan 1,4-alpha-glucosidase
3204	6704	3106970	3106053	918						
3205	6705	3107769	3106951	819	sp-GLPQ_BACSU	Bacillus subtilis glpQ	29.0	54.1	259	glycerophosphoryl diester phosphodiesterase
3206	6706	3108131	3108519	1389	sp-GLPQ_BACSU	Bacillus subtilis gmp	37.3	71.9	456	glucuronate permease
3207	6707	3108454	3108823	642						
3208	6708	3108845	3110003	159						
3209	6709	3112080	3110464	1617	sp-KPVK_CORGL	Corynebacterium glutamicum AS019 pyk	25.5	47.7	491	pyruvate kinase
3210	6710	3113390	3112449	942	gsp-Y25997	Brevibacterium flavum tda	99.7	99.7	314	L-lactate dehydrogenase
3211	6711	3113619	3115394	1776	pir-C70893	Mycobacterium tuberculosis H37RV RY1089c	33.5	64.8	526	hypothetical protein
3212	6712	3115407	3116042	636	gp-SC1C2_30	Streptomyces coelicolor A3(2) SCTC2_30	32.1	58.5	224	hydrolase or haloacid dehalogenase-like hydrolase
3213	6713	3116079	3116821	543	gp-AF030288_1	Brevibacterium linens ORF-1 ImpA	39.9	67.6	188	efflux protein
3214	6714	3116640	3117332	683	sp-GLCC_ECOLI	Escherichia coli K12 MG1655 glcC	27.6	57.0	221	transcription activator or transcriptional regulator GntR family
3215	6715	3117336	3118121	786	pir-B70885	Mycobacterium tuberculosis H37RV R2759c	47.8	68.6	255	phosphatase
3216	6716	3118254	3118582	1299	sp-SHIA_ECOLI	Escherichia coli K12 shiA	37.9	74.4	422	shikimate transport protein